

(i) APPLICANT: Flohé, Leopold
Singh, Mahavir
Hutter, Bernd
Kolk, Arend

(ii) TITLE OF INVENTION: Test-Kit For Tuberculosis Diagnosis etc.

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
- (B) STREET: 233 South Wacker Drive/6300 Sears Tower
- (C) CITY: Chicago
- (D) STATE: Illinois
- (E) COUNTRY: United States of America
- (F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/EP98/00483
(B) FILING DATE: 29-JAN-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 97101338.8
(B) FILING DATE: 29-JAN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Zeller, James P.
(B) REGISTRATION NUMBER: 28,491
(C) REFERENCE/DOCKET NUMBER: 29473/35834

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (312) 474-6300
(B) TELEFAX: (312) 474-0448

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1260 base pairs

[illegible]

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTC	CCCAT	CAGCAATCTT	GCAGATTAAT	CGAACTTTCT	TCACACTGAA	GCGTACAGTA	60
TCGAGAGGGG	TAATCATGCG	CGTCGGTATT	CCGACCGAGA	CCAAAAACAA	CGAATTCCAA		120
TTCCGGGTGG	CCATCACCCC	GGCCGGCGTC	GCGGAACTAA	CCCGTCGTGG	CCATGAGGTG		180
CTCATCCAGG	CAGGTGCCGG	AGAGGGCTCG	GCTATCACCG	ACGCGGATTT	CAAGGCGGCA		240
GGCGCGCAAC	TGGTCGGCAC	CGCCGACCAG	GTGTGGGCCG	ACGCTGATTT	ATTGCTCAAG		300
GTCAAAGAAC	CGATAGCGGC	GGAATACGGC	CGCCTGCGAC	ACGGGCAGAT	CTTGTTACAG		360
TTCTTGCAAT	TGGCCGCGTC	ACGTGCTTGC	ACCGATGCGT	TGTTGGATTC	CGGCACCACG		420
TCAATTGCCT	ACGAGACCGT	CCAGACCGCC	GACGGCGCAC	TACCCCTGCT	TGCCCCGATG		480
AGCGAAGTCG	CCGGTCGACT	CGCCGCCCAG	GTTGGCGCTT	ACCACCTGAT	GCGAACCCTAA		540
GGGGGCCGCG	GTGTGCTGAT	GGGCGGGGTG	CCCGGCGTCG	AACCGGCCGA	CGTCGTGGTG		600
ATCGGCGCCG	GCACCGCCGG	CTACAACGCA	GCCCGCATCG	CCAACGGCAT	GGGCGCGACC		660
GTTACGGTTC	TAGACATCAA	CATCGACAAA	CTTCGGCAAC	TCGACGCCGA	GTTCTGCGGC		720
CGGATCCACA	CTCGCTACTC	ATCGGCCTAC	GAGCTCGAGG	GTGCCGTCAA	ACGTGCCGAC		780
CTGGTGATTG	GGGCCGTCCT	GGTGCCAGGC	GCCAAGGCAC	CCAAATTAGT	CTCGAATTCA		840
CTTGTCGCGC	ATATGAAACC	AGGTGCGGTA	CTGGTGGATA	TAGCCATCGA	CCAGGGCGGC		900
TGTTTCGAAG	GCTCACGACC	GACCACCTAC	GACCACCCGA	CGTTCGCCGT	GCACGACACG		960
CTGTTTTACT	GCGTGGCGAA	CATGCCCCGC	TCGGTGCCGA	AGACGTGCAC	CTACGCGCTG		1020
ACCAACGCGA	CGATGCCGTA	TGTGCTCGAG	CTTGCCGACC	ATGGCTGGCG	GGCGGCGTGC		1080
CGGTCTGAATC	CGGCACTAGC	CAAAGGTCTT	TCGACGCACG	AAGGGGCGTT	ACTGTCCGAA		1140
CGGGTGGCCA	CCGACCTGGG	GGTGCCGTTC	ACCGAGCCCG	CCAGCGTGCT	GGCCTGACTC		1200

(2) INFORMATION FOR SEO ID NO:2:

(A) LENGTH: 1245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATCTTGCAGA	TTAATCGAAC	TTTCTTCACA	CTGAAGCGTA	CAGTATCGAG	AGGGGTAATC	60
ATGCGCGTCG	GTATTCCGAC	CGAGACCAAA	AACAACGAAT	TCCAATTCCG	GGTGGCCATC	120
ACCCCGGCCG	GCGTCGCGGA	ACTAACCCGT	CGTGGCCATG	AGGTGCTCAT	CCAGGCAGGT	180
GCCGGAGAGG	GCTCGGCTAT	CACCGACGCG	GATTTCAAGG	CGGCAGGCGC	GCAACTGGTC	240
GGCACC GCCG	ACCAGGTGTG	GGCCGACGCT	GATTTATTGC	TCAAGGTCAA	AGAACCGATA	300
GCGGCGGAAT	ACGGCCGCCT	GCGACACGGG	CAGATCTTGT	TCACGTTCTT	GCATTTGGCC	360
GCGTCACGTG	CTTGCAACCGA	TGCGTTGTTG	GATTCCGGCA	CCACGTCAAT	TGCCTACGAG	420
ACCGTCCAGA	CCGCCGACGG	CGCACTACCC	CTGCTTGCCC	CGATGAGCGA	AGTCGCCGGT	480
CGACTCGCCG	CCCAGGTTGG	CGCTTACCAC	CTGATGCGAA	CCCAAGGGGG	CCGCGGTGTG	540
CTGATGGGCG	GGGTGCCCCG	CGTCGAACCG	GCCGACGTCG	TGGTGATCGG	CGCCGGCACC	600
GCCGGCTACA	ACGCAGCCCC	CATCGCCAAC	GGCATGGGCG	CGACCGTTAC	GGTTC TAGAC	660
ATCAACATCG	ACAAACTTCG	GCAACTCGAC	GCCGAGTTCT	GCGGCCGGAT	CCACACTCGC	720
TACTCATCGG	CCTACGAGCT	CGAGGGTGCC	GTCAAACGTG	CCGACCTGGT	GATTGGGGCC	780
GTCCTGGTGC	CAGGCGCCAA	GGCACCCAAA	TTAGTCTCGA	ATTCACTTGT	CGCGCATATG	840
AAACCAGGTG	CGGTACTGGT	GGATATAGCC	ATCGACCAGG	GCGGCTGTTT	CGAAGGCTCA	900
CGACCGACCA	CCTACGACCA	CCCGACGTTT	GCCGTGCACG	ACACGCTGTT	TTACTGCGTG	960
GCGAACATGC	CCGCCTCGGT	GCCGAAGACG	TCGACCTACG	CGCTGACCAA	CGCGACGATG	1020

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 1235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATCTTGCAGA	TTAATCGAAC	TTTCTTCACA	CTGAAGCGTA	CAGTATCGAG	AGGGGTAATC	60
ATGCGCGTCG	GTATTCCGAC	CGAGACCAAA	AACAACGAAT	TCCGGGTGGC	CATCACCCCG	120
GCCGGCGTCG	CGGAAC TAAC	CCGTCGTGGC	CATGAGGTGC	TCATCCAGGC	AGGTGCCCGA	180
GAGGGCTCGG	CTATCACCGA	CGCGGATTTC	AAGGCGGCAG	GCGCGCAACT	GGTCGGCACC	240
GCCGACCAGG	TGTGGGCCGA	CGCTGATTTA	TTGCTCAAGG	TCAAAGAACC	GATAGCGGCG	300
GAATACGGCC	GCCTGCGACA	CGGGCAGATC	TTGTTCACGT	TCTTGCATTT	GGCCGCGTCA	360
CGTGCTTGCA	CCGATGCGTT	GTTGGATTCC	GGCACCACGT	CAATTGCCTA	CGAGACCGTC	420
CAGACCGCCG	ACGGCGCACT	ACCCCTGCTT	GCCCCGATGA	GCGAAGTCGC	CGGTGCGACTC	480
GCCGCCCAGG	TTGGCGCTTA	CCACCTGATG	CGAACCCAAG	GGGGCCGCGG	TGTGCTGATG	540
GGCGGGGTGC	CCGGCGTCGA	ACCGGCCGAC	GTCGTGGTGA	TCGGCGCCGG	CACCGCCGGC	600
TACAACGCAG	CCCGCATCGC	CAACGGCATG	GGCGCGACCG	TTACGGTTCT	AGACATCAAC	660
ATCGACAAAC	TTCGGCAACT	CGACGCCGAG	TTCTGCGGCC	GGATCCACAC	TCGCTACTCA	720
TCGGCCTACG	AGCTCGAGGG	TGCCGTCAAA	CGTGCCGACC	TGGTGATTGG	GGCCGTCCTG	780
GTGCCAGGCG	CCAAGGCACC	CAAATTAGTC	TCGAATTAC	TTGTGCGGCA	TATGAAACCA	840

GGTGCGGTAC TGGTGGATAT AGCCATCGAC CAGGGCGGCT GTTTCGAAGG CTCACGACCG 900
ACCACCTACG ACCACCCGAC GTTCGCCGTG CACGACACGC TGTTTTACTG CGTGGCGAAC 960
ATGCCCCCCT CGGTGCCGAA GACGTCGACC TACGCGCTGA CCAACGCGAC GATGCCGTAT 1020
GTGCTCGAGC TTGCCGACCA TGGCTGGCGG GCGGCGTGCC GGTCGAATCC GGCAC TAGCC 1080
AAAGGTCTTT CGACGCACGA AGGGGCGTTA CTGTCCGAAC GGGTGGCCAC CGACCTGGGG 1140
GTGCCGTTCA CCGAGCCCGC CAGCGTGCTG GCCTGACTCT CGGCCGCTCG TTACGCCGAG 1200
CACACNTCGG GAGTAANGGA AGCGATGATG TCGNC 1235

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCTTGCAGA TTAATCGAAC TTTCTTCATA CTGAAGCGTA CAGTATCGAG AGGGGTAATC 60
ATGCGCGTCG GTATTCCGAC CGAGACCAAA AACAAACGAAT TCCGGGTGGC CATCACCCCG 120
GCCGGCGTCG CGGAACTAAC CCGTCGTGGC CATGAGGTGC TCATCCAGGC AGGTGCCGGA 180
GAGGGCTCGG CTATCACCGA CGCGGATTTC AAGGCGGCAG GCGCGCAACT GGTGCGCACC 240
GCCGACCAGG TGTGGGCCGA CGCTGATTTA TTGCTCAAGG TCAAAGAACC GATAGCGGCG 300
GAATACGGCC GCCTGCGACA CGGGCAGATC TTGTTACGT TCTTGCAATT GGCCGCGTCA 360
CGTGCTTGCA CCGATGCGTT GTTGGATTCC GGCACCACGT CAATTGCCTA CGAGACCGTC 420
CAGACCGCCG ACGGCGCACT ACCCCTGCTT GCCCCGATGA GCGAAGTCGC CGGTCGACTC 480
GCCGCCAGG TTGGCGCTTA CCACCTGATG CGAACCCAAG GGGGCCGCGG TGTGCTGATG 540
GGCGGGGTGC CCGGCGTCGA ACCGGCCGAC GTCGTGGTGA TCGGCGCCGG CACCGCCGGC 600
TACAACGCAG CCCGCATCGC CAACGGCATG GGCGCGACCG TTACGGTTCT AGACATCAAC 660

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 1228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATCTTGCAGA	TTAATCGAAC	TTTCTTCATA	CTGAAGCGTA	CAGTATCGAG	AGGGGTAATC	60
ATGCGCGTCG	GTATTCCGAC	CGAGACCAAA	AACAACGAAT	TCCGGGTGGC	CATCACCCCG	120
GCCGGCGTCG	CGGAACTAAC	CCGTCGTGGC	CATGAGGTGC	TCATCCAGGC	AGGTGCCCGA	180
GAGGGCTCGG	CTATCACCGA	CGCGGATTTC	AAGGCGGCAG	GCGCGCAACT	GGTCGGCACC	240
GCCGACCAGG	TGTGGGCCGA	CGCTGATTTA	TTGCTCAAGG	TCAAAGAACC	GATAGCGGCG	300
GAATACGGCC	GCCTGCGACA	CGGGCAGATC	TTGTTCACGT	TCTTGCATTT	GGCCGCGTCA	360
CGTGCTTGCA	CCGATGCGTT	GTTGGATTCC	GGCACCACGT	CAATTGCCTA	CGAGACCGTC	420
CAGACCGCCG	ACGGCGCACT	ACCCCTGCTT	GCCCCGATGA	GCGAAGTCGC	CGGTGCGACTC	480

GCCGCCCAGG TTGGCGCTTA CCACCTGATG CGAACCCAAG GGGGCCGCGG TGTGCTGATG 540
GGCGGGGTGC CCGGCGTCGA ACCGGCCGAC GTCGTGGTGA TCGGCGCCGG CACCGCCGGC 600
TACAACGCAG CCCGCATCGC CAACGGCATG GGCGCGACCG TTACGGTTCT AGACATCAAC 660
ATCGACAAAC TTCGGCAACT CGACGCCGAG TTCTGCGGCC GGATCCACAC TCGCTACTCA 720
TCGGCCTACG AGCTCGAGGG TGCCGTCAA CCGTCCGACC TGGTGATTGG GGCCGTCCTG 780
GTGCCAGGCG CCAAGGCACC CAAATTAGTC TCGAATTCAC TTGTGCGCA TATGAAACCA 840
GGTGCGGTAC TGGTGGATAT AGCCATCGAC CAGGGCGGCT GTTTCGAAGG CTCACGACCG 900
ACCACCTACG ACCACCCGAC GTTCGCCGTG CACGACACGC TGTTTTACTG CGTGGCGAAC 960
ATGCCCCCCT CGGTGCCGAA GACGTCGACC TACGCGCTGA CCAACGCGAC GATGCCGTAT 1020
GTGCTCGAGC TTGCCGACCA TGGCTGGCGG GCGGCGTGCC GGTCGAATCC GGCCTAGCC 1080
AAAGGTCTTT CGACGCACGA AGGGGCGTTA CTGTCCGAAC GGGTGGCCAC CGACCTGGGG 1140
GTGCCGTTCA CCGAGCCCCG CAGCGTGCTG GCCTGACTCT CGGCCGCTCG TTACGCCGAG 1200
CACACGTCGG GAGTAAGGGA AGCGATGA 1228

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATCTTGCAGA TTAATCGAAC TTTCTTCACA CTGAAGCGTA CAGTATCGAG AGGGGTAATC 60
ATGCGCGTCG GTATTCCGAC CGAGACCAA AACAACGAAT TCCGGGTGGC CATCACCCCG 120
GCCGGCGTCG CGGAACTAAC CCGTCGTGGC CATGAGGTGC TCATCCAGGC AGGTGCCGGA 180
GAGGGCTCGG CTATCACCGA CGCGGATTTC AAGGCGGCAG GCGCGCAACT GGTCGGCACC 240
GCCGACCAGG TGTGGGCCGA CGCTGATTTA TTGCTCAAGG TCAAAGAACC GATAGCGGCG 300

GAATACGGCC GCCTGCGACA CGGGCGATCT TGTTACGTT CTTGCATTTG GCCGCGTCAC 360
GTGCTTGAC CGATGCGTTG TTGGATTCCG GCACCACGTC AATTGCCTAC GAGACCGTCC 420
AGACCGCCGA CGGCGCACTA CCCCTGCTTG CCCCAGATGAG CGAAGTCGCC GGTGCGACTCG 480
CCGCCCAGGT TGGCGCTTAC CACCTGATGC GAACCCAAGG GGGCCGCGGT GTGCTGATGG 540
GCGGGGTGCC CGGCGTCGAA CCGGCCGACG TCGTGGTGAT CGGCGCCGGC ACCGCCGGCT 600
ACAACGCAGC CCGCATCGCC AACGGCATGG GCGCGACCGT TACGGTTCTA GACATCAACA 660
TCGACAAACT TCGGCAACTC GACGCCGAGT TCTGCGGCCG GATCCACACT CGTACTCAT 720
CGGCCTACGA GCTCGAGGGT GCCGTCAAAC GTGCCGACCT GGTGATTGGG GCCGTCTTGG 780
TGCCAGGCGC CAAGGCACCC AAATTAGTCT CGAATTCAC TGTGCGCAT ATGAAACCAG 840
GTGCGGTACT GGTGGATATA GCCATCGACC AGGGCGGCTG TTTCGAAGGC TCACGACCGA 900
CCACCTACGA CCACCCGACG TTCGCCGTGC ACGACACGCT GTTTTACTGC GTGGCGAACA 960
TGCCCGCCTC GGTGCCGAAG ACGTCGACCT ACGCGCTGAC CAACGCGACG ATGCCGTATG 1020
TGCTCGAGCT TGCCGACCAT GGCTGGCGGG CGGCGTGCCG GTCGAATCCG GCACTAGCCA 1080
AAGGTCTTTC GACGCACGAA GGGGCGTTAC TGTCCGAACG GGTGGCCACC GACCTGGGGG 1140
TGCCGTTCAC CGAGCCCGCC AGCGTGCTGG CCTGACTCTC GGCCGCTCGT TACGCCGANC 1200
ACACGTCGGG AGTAAGGGAA GCGATGATGT CGGCC 1235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCTTGACAG TTAATCGAAC TTTCTTCACA CTGAAGCGTA CAGTATCGAG AGGGGTAATC 60
ATGCGCGTCG GTATTCCGAC CGAGACCAAA AACAACGAAT TCCGGGTGGC CATCACCCCG 120

GCCGGCGTCG	CGGAACAAAC	CCGTCGTGGC	CATGAGGTGC	TCATCCAGGC	AGGTGCCGGA	180
GAGGGCTCGG	CTATCACCGA	CGCGGATTTC	AAGGCGGCAG	GCGCGCAACT	GGTCGGCACC	240
GCCGACCAGG	TGTGGGCCGA	CGCTGATTTA	TTGCTCAAGG	TCAAAGAACC	GATAGCGGCG	300
GAATACGGCC	GCCTGCGACA	CGGGCGATCT	TGTTACAGTT	CTTGCAATTTG	GCCGCGTCAC	360
GTGCTTGAC	CGATGCGTTG	TTGGATTCCG	GCACCACGTC	AATTGCCTAC	GAGACCGTCC	420
AGACCGCCGA	AGGCGCACTA	CCCCTGCTTG	CCCCGATGAG	CGAAGTCGCC	GGTCGACTCG	480
CCGCCCAGGT	TGGCGCTTAC	CACCTGATGC	GAACCCAAGG	GGGCCGCGGT	GTGCTGATGG	540
GCGGGGTGCC	CGGCGTCGAA	CCGGCCGACG	TCGTGGTGAT	CGGCGCCGGC	ACCGCCGGCT	600
ACAACGCAGC	CCGCATCGCC	AACGGCATGG	GCGCGACCGT	TACGGTTCTA	GACATCAACA	660
TCGACAAACT	TCGGCAACTC	GACGCCGAGT	TCTGCGGCCG	GATCCACACT	CGTACTCAT	720
CGGCCTACGA	GCTCGAGGGT	GCCGTCAAAC	GTGCCGACCT	GGTGATTGGG	GCCGTCTTGG	780
TGCCAGGCGC	CAAGGCACCC	AAATTAGTCT	CGAATTCACT	TGTCGCGCAT	ATGAAACCAG	840
GTGCGGTACT	GGTGATATA	GCCATCGACC	AGGGCGGCTG	TTTCAAGGC	TCACGACCGA	900
CCACCTACGA	CCACCCGACG	TTCGCCGTGC	ACGACACGCT	GTTTTACTGC	GTGGCGAACA	960
TGCCCCCCTC	GGTGCCGAAG	ACGTCGACCT	ACGCGCTGAC	CAACGCGACG	ATGCCGTATG	1020
TGCTCGAGCT	TGCCGACCAT	GGCTGGCGGG	CGGCGTGCCG	GTCGAATCCG	GCACTAGCCA	1080
AAGGTCTTTC	GACGCACGAA	GGGGCGTTAC	TGTCCGAACG	GGTGGCCACC	GACCTGGGGG	1140
TGCCGTTTAC	CGAGCCCGCC	AGCGTGCTGG	CCTGACTCTC	GGCCGCTCGT	TACGCCGAGC	1200
ACACGTCNGG	AGTAAGGGAA	GCGATGATG				1229

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATCTTGCAGA	TTAATCGAAC	TTTCTTCACA	CTGAAGCGTA	CAGTATCGAG	AGGGGTAATC	60
ATGCGCGTCG	GTATTCCGAC	CGAGACCAAA	AACAACGAAT	TCCGGGTGGC	CATCACCCCG	120
GCCGGCGTCG	CGGAAC TAAC	CCGTCGTGGC	CATGAGGTGC	TCATCCAGGC	AGGTGCCGGA	180
GAGGGCTCGG	CTATCACCGA	CGCGGATTTC	AAGGCGGCAG	GCGCGCAACT	GGTCGGCACC	240
GCCGACCAGG	TGTGGGCCGA	CGCTGATTTA	TTGCTCAAGG	TCAAAGAACC	GATAGCGGCG	300
GAATACGGCC	GCCTGCGACA	CGGGCGATCT	TGTTACGTT	CTTGCAATTG	GCCGCGTCAC	360
GTGCTTGAC	CGATGCGTTG	TTGGATTCCG	GCACCACGTC	AATTGCCTAC	GAGACCGTCC	420
AGACCGCCGA	AGGCGCACTA	CCCCTGCTTG	CCCCGATGAG	CGAAGTCGCC	GGTCGACTCG	480
CCGCCCAGGT	TGGCGCTTAC	CACCTGATGC	GAACCCAAGG	GGGCCGCGGT	GTGCTGATGG	540
GCGGGGTGCC	CGGCGTCGAA	CCGGCCGACG	TCGTGGTGAT	CGGCGCCGGC	ACCGCCGGCT	600
ACAACGCAGC	CCGCATCGCC	AACGGCATGG	GCGCGACCGT	TACGGTTCTA	GACATCAACA	660
TCGACAAACT	TCGGCAACTC	GACGCCGAGT	TCTGCGGCCG	GATCCACACT	CGCTACTCAT	720
CGGCCTACGA	GCTCGAGGGT	GCCGTCAAAC	GTGCCGACCT	GGTGATTGGG	GCCGTCCTGG	780
TGCCAGGCGC	CAAGGCACCC	AAATTAGTCT	CGAATTCACT	TGTCGCGCAT	ATGAAACCAG	840
GTGCGGTACT	GGTGGATATA	GCCATCGACC	AGGGCGGCTG	TTTCGAAGGC	TCACGACCGA	900
CCACCTACGA	CCACCCGACG	TTGCCCGTGC	ACGACACGCT	GTTTTACTGC	GTGGCGAACA	960
TGCCCCGCTC	GGTGCCGAAG	ACGTCGACCT	ACGCGCTGAC	CAACGCGACG	ATGCCGTATG	1020
TGCTCGAGCT	TGCCGACCAT	GGCTGGCGGG	CGGCGTGCCG	GTCGAATCCG	GCTAGCCA	1080
AAGGTCTTTC	GACGCACGAA	GGGGCGTTAC	TGTCCGAACG	GGTGGCCACC	GACCTGGGGG	1140
TGCCGTTTAC	CGAGCCCGCC	AGCGTGCTGG	CCTGACTCTC	GGCCGCTCGT	TACGCCGAGC	1200
ACACGTCGGG	AGTAAGGGAA	GCGATGATGT	CGGCC			1235

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATCTTGCAGA	TTAATCGAAC	TTTCTTCACA	CTGAAGCGTA	CAGTATCGAG	AGGGGTAATC	60
ATGCGCGTCG	GTATTCCGAC	CGAGACCAAA	AACAACGAAT	TCCGGGTGGC	CATCACCCCG	120
GCCGGCGTCG	CGGAAC TAAC	CCGTCTGGC	CATGAGGTGC	TCATCCAGGC	AGGTGCCGGA	180
GAGGGCTCGG	CTATCACCGA	CGCGGATTTC	AAGGCGGCAG	GCGCGCAACT	GGTCGGCACC	240
GCCGACCAGG	TGTGGGCCGA	CGCTGATTTA	TTGCTCAAGG	TCAAAGAACC	GATAGCGGCG	300
GAATACGGCC	GCCTGCGACA	CGGGCAGATC	TTGTTCACGT	TCTTGCA TTT	GGCCGCGTCA	360
CGTGCTTGCA	CCGATGCGTT	GTTGGATTCC	GGCACCACGT	CAATTGCCTA	CGAGACCGTC	420
CAGACCGCCG	ACGGCGCACT	ACCCCTGCTT	GCCCCGATGA	GCGAAGTCGC	CGGTGCACTC	480
GCCGCCAGG	TTGGCGCTTA	CCACCTGATG	CGAACCCAAG	GGGGCCGCGG	TGTGCTGATG	540
GGCGGGGTGC	CCGGCGTCGA	ACCGGCCGAC	GTCGTGGTGA	TCGGCGCCGG	CACCGCCGGC	600
TACAACGCAG	CCCGCATCGC	CAACGGCATG	GGCGCGACCG	TTACGGTTCT	AGACATCAAC	660
ATCGACAAAC	TTCGGCAACT	CGACGCCGAG	TTCTGCGGCC	GGATCCACAC	TCGCTACTCA	720
TCGGCCTACG	AGCTCGAGGG	TGCCGTCAAA	CGTGCCGACC	TGGTGATTGG	GGCCGTCCTG	780
GTGCCAGGCG	CCAAGGCACC	CAAATTAGTC	TCGAATTCAC	TTGTCGCGCA	TATGAAACCA	840
GGTGCGGTAC	TGGTGGATAT	AGCCATCGAC	CAGGGCGGCT	GTTTCGAAGG	CTCACGACCG	900
ACCACCTACG	ACCACCCGAC	GTTCCGCCGTG	CACGACACGC	TGTTTTACTG	CGTGGCGAAC	960
ATGCCCCCCT	CGGTGCCGAA	GACGTCGACC	TACGCGCTGA	CCAACGCGAC	GATGCCGTAT	1020
GTGCTCGAGC	TTGCCGACCA	TGGCTGGCGG	GCGGCGTGCC	GGTCGAATCC	GGCACTAGCC	1080
AAAGGTCTTT	CGACGCACGA	AGGGGCGTTA	CTGTCCGAAC	GGGTGGCCAC	CGACCTGGGG	1140
GTGCCGTTCA	CCGAGCCCGC	CAGCGTGCTG	GCCTGACTCT	CGGCCGCTCG	TTACGCCGAG	1200
CNCACGTCG						1209

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1236 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCTTGCAGA	TTAATCGAAC	TTTCTTCACA	CTGAAGCGTA	CAGTATCGAG	AGGGGTAATC	60
ATGCGCGTCG	GTATTCCGAC	CGAGACCAAA	AACAACGAAT	TCCGGGTGGC	CATCACCCCG	120
GCCGGCGTCG	CGGAACTAAC	CCGTCGTGGC	CATGAGGTGC	TCATCCAGGC	AGGTGCCGGA	180
GAGGGCTCGG	CTATCACCGA	CGCGGATTTC	AAGGCGGCAG	GCGCGCAACT	GGTCGGCACC	240
GCCGACCAGG	TGTGGGCCGA	CGCTGATTTA	TTGCTCAAGG	TCAAAGAACC	GATAGCGGCG	300
GAATACGGCC	GCCTGCGACA	CGGGCAGATC	TTGTTCACGT	TCTTGCATTT	GGCCGCGTCA	360
CGTGCTTGCA	CCGATGCGTT	GTTGGATTCC	GGCACCACGT	CAATTGCCTA	CGAGACCGTC	420
CAGACCGCCG	ACGGCGCACT	ACCCCTGCTT	GCCCCGATGA	GCGAAGTCGC	CGGTGCACTC	480
GCCGCCCAGG	TTGGCGCTTA	CCACCTGATG	CGAACCCTAAG	GGGGCCGCGG	TGTGCTGATG	540
GGCGGGGTGC	CCGGCGTCGA	ACCGGCCGAC	GTCGTGGTGA	TCGGCGCCGG	CACCGCCGGC	600
TACAACGCAG	CCCGCATCGC	CAACGGCATG	GGCGCGACCG	TTACGGTTCT	AGACATCAAC	660
ATCGACAAAC	TTCGGCAACT	CGACGCCGAG	TTCTGCGGCC	GGATCCACAC	TCGCTACTCA	720
TCGGCCTACG	AGCTCGAGGG	TGCCGTCAAA	CGTGCCGACC	TGGTGATTGG	GGCCGTCCTG	780
GTGCCAGGCG	CCAAGGCACC	CAAATTAGTC	TCGAATTCAC	TTGTGCGGCA	TATGAAACCA	840
GGTGCGGTAC	TGGTGGATAT	AGCCATCGAC	CAGGGCGGCT	GTTTCGAAGG	CTCACGACCG	900
ACCACCTACG	ACCACCCGAC	GTTCGCCGTG	CACGACACGC	TGTTTTACTG	CGTGGCGAAC	960
ATGCCCCGCT	CGGTGCCGAA	GACGTCGACC	TACGCGCTGA	CCAACGCGAC	GATGCCGTAT	1020
GTGCTCGAGC	TTGCCGACCA	TGGCTGGCGG	GCGGCGTGCC	GGTCGAATCC	GGCACTAGCC	1080
AAAGGTCTTT	CGACGCACGA	AGGGGCGTTA	CTGTCCGAAC	GGGTGGCCAC	CGACCTGGGG	1140
GTGCCGTTCA	CCGAGCCCGC	CAGCGTGCTG	GCCTGACTCT	CGGCCGCTCG	TTACGCCGAG	1200
CACACGTCGG	GAGTAAGGGA	AGCGATGATG	TCGGCC			1236

09062405:072909

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

18

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGACCAAAA ACAACGAA

18

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCCCAT CAGCAATCTT GCAGA

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCCCGATGA GCGAAGTC

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

66320:5842960

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGGCCGTCC TGGTGCC

17

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACGTCGACC TACGCGCTGA C

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

0936495:072809

CTCGGTGAAC GGCACCCC

18

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCCAGCACG CTGGCGGG

18

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CACCCGTTTCG GACAGTAA

18

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

BBB20:542960

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGGCCGAC ATCATCGC

18

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCCGACATC ATCGCTTCCC

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGAGACTAAT TTGGGTGCCT TGGC

24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs

666220-58429660

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATTTGGGTGC CTTGGC

16

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGCGGCGAGT CGACCGGC

18

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

663220-5423650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGAATTCC AATTCCGGGT G

21

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asn Glu Phe Gln Phe Arg Val
1 5

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AACGAATTCC GGGTG

15

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 20 -

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn	Glu	Phe	Arg	Val
1				5

0932485-072899